Chirag Gupta

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SUMMARY

Bioinformatics Scientist with 8+ years of experience in high-throughput genomic data analysis, data-driven scientific investigations in multiple species, and bioinformatics tool development. My objective is to develop methods for integrating the vast amounts of continuously accumulating high-throughput -omics data, for the purposes of developing **predictive machine learning models** and platforms that will enable wet lab scientists design effective downstream experiments. I have extensive experience in written and oral communication to academics and business leaders through 10+ peer reviewed publications, 4+ oral and 10+ poster presentations.

EDUCATION

2017	**Ph.D. Cell and Molecular Biology (Computational)** Dissertation: Transcriptome-based gene networks for systems-level analysis of gene function in plants	**University of Arkansas** Fayetteville, AR
2009	**M.Sc. Bioinformatics**	**Sardar Patel University, India**
2007	**B.Sc. Bioinformatics**	**Sardar Patel University, India**

RESEARCH EXPERIENCE

2017 — present **Postdoctoral Research Associate** — **University of Arkansas**, Fayetteville, AR

- Created the DroughtApp, a machine-learning based gene recommender platform that enables prioritization of likely candidates for the CRISPR pipeline in rice
- Optimized a pipeline to detect high-quality SNPs and other structural variants in NGS data by rigorous testing of several competing software
- Mentored other scientists within and outside the core lab through technical assistance and efficient data analysis infrastructure

2012 — 2017 **Graduate Research Assistant** — **University of Arkansas**, Fayetteville, AR

- Built genome-scale co-expression networks in rice and Arabidopsis for context-specific function predictions, leading to updated ontologies and discovery of novel trait genes
- Created two interactive webtools that can help users to visualize and analyze co-expression networks in model plant species
- Played a key role in development of two winning grants, and established several external collaborations

2008 — 2009 **Student Researcher** — **Disha Life Sciences Pvt. Ltd**, Ahmedabad, India

- Identified genomic and protein structure attributes of a fusion-protein involved in leukemia
- Screened natural product libraries for bioactive molecules using molecular docking tools
- Generated insilico models of lead molecules for pre-clinical drug development

PUBLICATIONS

Under review/preprints

1) **Chirag Gupta**, Venkategowda Ramegowda, Supratim Basu, Andy Pereira. Prediction and characterization of transcription factors involved in drought stress response bioRxiv, doi: 10.1101/2020.04.29.068379 (*under review at plant physiology)*

2) **Chirag Gupta**, Arjun Krishnan, Andrew Schneider, Cynthia Denbow, Eva Collakova, Pawel Wolinski, Andy Pereira. SANe: The Seed Active Network for Discovering Transcriptional Regulatory Programs of Seed Development. bioRxiv, doi: 10.1101/165894 *(The platform is currently being updated to add multiple plant species)*

Peer reviewed journal articles

1) Raksha Singh, Rohana Liyanage, **Chirag Gupta,** Jackson Lay Jr., Andy Pereira, Clemencia Rojas. The protein interactomes of AtNHR2A and AtNHR2B unraveled common and specialized functions in plant immunity integrating distinct biological processes. **Frontiers in Plant Science**, March 2020. doi: 10.3389/fpls.2020.00232.

2) Min Woo Lee, Carmen S. Padilla, **Chirag Gupta**, Aravind Galla, Andy Pereira, Jiamei Li, Fiona L. Goggin. The FATTY ACID DESATURASE 2 family in tomato contributes to primary metabolism and stress responses. **Plant Physiology**, Nov. 2019. doi:10.1104/pp.19.00487

3) **Chirag Gupta** and Andy Pereira. Recent advances in gene function prediction using context-specific coexpression networks in plants. **F1000Research**, Feb. 2019. doi: 10.12688/f1000research.17207.1.

4) Arjun Krishnan, **Chirag Gupta**, Madana MR Ambavaram, Andy Pereira. RECoN: Rice Environment Co-expression Network for systems level analysis of abiotic-stress response. **Frontiers in Plant Science**, Sep. 2017. doi: 10.3389/fpls.2017.01640

5) Venkategowda Ramegowda, Upinder Singh Gill, Palaiyur Nanjappan Sivalingam, Aarti Gupta, **Chirag Gupta**, Geetha Govind, Karaba N Nataraja, Andy Pereira, Makarla Udayakumar, Kirankumar S Mysore, Muthappa Senthil-Kumar. GBF3 transcription factor imparts drought tolerance in Arabidopsis thaliana. **Scientific Reports**, August 2017. doi: 10.1038/s41598-017-09542-1.

6) Venkategowda Ramegowda, Supratim Basu, **Chirag Gupta**, Andy Pereira. Regulation of grain yield in rice under well-watered and drought stress conditions by GUDK. **Plant Signaling and Behavior**, January 2015. doi: 10.1080/15592324.2015.1034421.

Published project reports

1) Anuj Kumar, Sara Yingling, Julie Thomas, Charles Ruiz, Yheni Dwiningsih, **Chirag Gupta**, Paul Counce, T.J. Siebenmorgen, Karen A.K. Moldenhauer, Andy Pereira. Screening of Indica and Japonica rice subspecies for grain yield and quality under high nighttime temperature. **B.R. Wells Arkansas Rice Research Studies 2018**, 659:61-66.

2) Ramegowda Venkategowda, Subodh Srivastava, Julie Thomas, **Chirag Gupta**, Supratim Basu, Paul Counce, Ya-Jane Wang, Terry Siebenmorgen, Karen Moldenhauer, Andy Pereira. Genetic basis of altered grain quality in different rice cultivars under high nighttime temperature. **B.R. Wells Arkansas Rice Research Studies 2015,** 634:79-85.

CONFERENCE PRESENTATIONS

Talks

- Predicting rice genes important for drought tolerance using gene regulatory networks and machine learning. **Crops InSilico, 4th Annual Symposium and Hackathon**, Urbana, IL, 3rd May 2019
- Arabidopsis seed-filling association-network analysis. **American Society of Plant Biologists – Southern Section (ASPB-SS)**, Lexington, KY, 30th March 2014

Select posters

- Network-based approach to prioritize lung cancer genes from whole-exome sequencing data. **AR-BIC**, Little Rock, AR, 25th March 2018
- Differential Co-expression: A new paradigm for identification of candidate genes from expression data. **AR-BIC**, Little Rock, AR, 24th April 2017
- An abiotic-stress conditioned gene regulatory network in rice predicted using an ensemble of reverse-engineering solutions. **The 25th Plant and Animal Genome (PAG) Conference,** San Diego, CA, 14th January 2017
- A resource for systems analysis of stress response in rice. **NSF Workshop on plant development and drought stress**, Monterey, CA, 8th November 2015
- StarchNet: Implications of high night-time temperature on starch metabolism regulatory networks in rice. **AR NSF EPSCoR Annual Meeting**, Fayetteville, AR, 15th September 2015
- In Silico Analysis of Fusion Proteins in Cancer, **International Conference on Biomedical and Genomic Research**, Ahmedabad, India, 30th January 2009

AWARDS

- Crops in silico underrepresented minority travel scholarship, **Crops InSilico**, Urbana, IL, 2019
- Scherago International Student Travel Grants Awards, **The 25th annual Plant and Animal Genome (PAG) meeting**, San Diego, CA, 2017
- NSF Travel Grant to attend the Workshop on Plant Development and Drought Stress, **National Science Foundation**, 2015
- Stood 3rd in merit list for all India entrance examination for Master's in bioinformatics program, **Sardar Patel University**, India, 2007
- 2nd Prize in undergraduate oral presentation, **Sardar Patel University**, India, 2006
- 3rd Prize in undergraduate poster competition, **Atmiya University**, India , 2006

CONTRIBUTION TO GRANTS

- **NSF EPSCoR RII Track-2 FEC 1826836**: Systems genetics studies on rice genomes for analysis of grain yield and quality under heat stress (PI: Dr. Andy Pereira; $4,659,406), 2018
- **NSF MCB 1716844**: Systems genetics analysis of photosynthetic carbon metabolism in rice (PI: Dr. Andy Pereira; $798,725.00), 2017

SOCIETY MEMBERSHIPS

2020 – present The International Society for Computational Biology (ISCB)

SELECT SKILLS

Programming	R, Perl, PHP, mySQL and JavaScript
Applications	Docker, STAR, Tuxedo suite, BWA, Samtools, GATK, Picard, VarScan, Mutect, SomaticSniper, VCFtools, edgeR, DESeq, limma, LibSVM, Weka, BLAST, Arguslab, MolSoft, Rasmol, I-TASSER etc.
Visualization	Shiny, CytoscapeWeb, D3.js
Platforms	UNIX, Linux, Google cloud, MacOS
Version control	Github

TOOLS DEVELOPED

DroughtApp	http://rrn.uark.edu/shiny/apps/rrn/
SANe	https://plantstress-pereira.uark.edu/SANe/
RECoN	https://plantstress-pereira.uark.edu/RECoN/

TEACHING EXPERIENCE

Co-taught Plant Genomics (**Bioinformatics/Genomics modules**: CSES 5543, Uni. Of Arkansas), 2016, 2018

EXTENSION ACTIVITIES

Student and Teacher Workshop: **rice genetic variation** (18 credit hours, Uni. Of Arkansas), 2019

ACADEMIC SERVICE

- **Manuscript reviewer** for Plant Physiology, Frontiers in Plant Science, Nature Scientific Reports, Rice, Plant Cell Reports
- **Plante Fellow 2019**: Contribution to the Plantae online portal for Bioinformatics resources relevant to plant biology research
- Member of the panel of judges for the **Northwest Arkansas Regional Science and Engineering Fair** 2015,16
- Conducted several training material and hands-on activities for undergraduates and K-12 students from the Arkansas agricultural areas in the Delta region for a **STEM literacy outreach program**

REFREES

Available upon request